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SEQUENCE LISTING

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Yasuaki Ito
Ryo Fujii

(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Edwards & Angell, LLP
(B) P.O. Box 9169
(C) CITY: BOSTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02209

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/461,436
(B) FILING DATE: 14-DECEMBER-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974
(B) FILING DATE: 14-SEP-1995

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(B) FILING DATE: 10-AUG-1995

(A) APPLICATION NUMBER: 7-093989
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(B) FILING DATE: 16-MAR-1995

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(B) FILING DATE: 20-JAN-1995

(A) APPLICATION NUMBER: 6-326611
(B) FILING DATE: 28-DEC-1994

(A) APPLICATION NUMBER: 6-270017
(B) FILING DATE: 02-NOV-1994

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(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: 6-189274

(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189273

(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189272

(B) FILING DATE: 11-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-439-4444

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG

25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAAA

27

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSGCMY TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRARRAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCMY TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ASNSANRAAG SARTAGANGA NRGGR TT 27

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNAA 25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWGGGSAKC CAGCASANGG CRAA 24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 15th N is A, G, C, or T
6th, 9th, 10th & 12th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY 18

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 13th, 15th, 16th & 18th Ns are
each A, G, C, or T
1st, 4th, 6th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

NGGNANCCAR CANANNRNRA A 21

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTNRN SATGWSTGTG GANMGNT 27

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA 27

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTTGCT GCCACAGGCA TCCAGCG 27

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGCAGCAAG 30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Leu | Val | Ile | Ala | Arg | Val | Arg | Arg | Leu | His | Asn | Val | Thr | Asn |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu | Ser | Asp | Val | Leu | Met | Cys | Thr | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr | Ala | Phe | Glu | Pro | Arg | Gly | Trp | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Phe | Gly | Gly | Gly | Leu | Cys | His | Leu | Val | Phe | Phe | Leu | Gln | Pro | Val | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Tyr | Val | Ser | Val | Phe | Thr | Leu | Thr | Thr | Ile | Ala | Val | Asp | Arg | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Val | Val | Leu | Val | His | Pro | Leu | Arg | Arg | Arg | Ile | | | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Leu | Leu | Val | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Val | Ile | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val | Val | Pro | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg | Arg | Arg | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | | | | | |
| | 50 | | | | | 55 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
1 5 10 15
Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
20 25 30
Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
35 40 45
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
50 55 60
Leu Leu Tyr Ser Val Val Val Val Gly Leu Val Gly Asn Cys Leu
65 70 75 80
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
85 90 95
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
100 105 110
Cys Val Pr

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

u Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
180 185 190

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
195 200 205

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
210 215 220

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
225 230 235 240

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 245 | | 250 | | 255 | | | | | | | | | | |
| Val | Pro | Gly | Cys | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Arg | Arg | Arg | Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Phe | Ala |
| | | | 275 | | | | 280 | | | | | 285 | | | |
| Val | Cys | Trp | Leu | Pro | Leu | His | Val | Phe | Asn | Leu | Leu | Arg | Asp | Leu | Asp |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Pro | His | Ala | Ile | Asp | Pro | Tyr | Ala | Phe | Gly | Leu | Val | Gln | Leu | Leu | Cys |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| His | Trp | Leu | Ala | Met | Ser | Ser | Ala | Cys | Tyr | Asn | Pro | Phe | Ile | Tyr | Ala |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Trp | Leu | His | Asp | Ser | Phe | Arg | Glu | Glu | Leu | Arg | Lys | Leu | Leu | Val | Ala |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Trp | Pro | Arg | Lys | Ile | Ala | Pro | His | Gly | Gln | Asn | Met | Thr | Val | Ser | Val |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Val | Ile | | | | | | | | | | | | | | |
| | 370 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Leu | Val | Ile | Ala | Arg | Val | Arg | Arg | Leu | Tyr | Asn | Val | Thr | Asn |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Phe | Leu | Ile | Gly | Asn | Leu | Ala | Leu | Ser | Asp | Val | Leu | Met | Cys | Thr | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Val | Pro | Leu | Thr | Leu | Ala | Tyr | Ala | Phe | Glu | Pro | Arg | Gly | Trp | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Phe | Gly | Gly | Gly | Leu | Cys | His | Leu | Val | Phe | Phe | Leu | Gln | Ala | Val | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Tyr | Val | Ser | Val | Phe | Thr | Leu | Thr | Thr | Ile | Ala | Val | Asp | Arg | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Val | Leu | Val | His | Pro | Leu | Arg | Arg | Arg | Ile | Ser | Leu | Arg | Leu | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Tyr | Ala | Val | Leu | Ala | Ile | Trp | Val | Leu | Ser | Ala | Val | Leu | Ala | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Pro | Ala | Ala | Val | His | Thr | Tyr | His | Val | Glu | Leu | Lys | Pro | His | Asp | Val |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Arg | Leu | Cys | Glu | Glu | Phe | Trp | Gly | Ser | Gln | Glu | Arg | Gln | Arg | Gln | Leu |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Tyr | Ala | Trp | Gly | Leu | Leu | Leu | Val | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Leu | Leu | Ser | Tyr | Ala | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Pro | Gly | Arg | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Arg | Arg | Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Val | |
| | | | 195 | | | | 200 | | | | | | 205 | | |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Leu | Val | His | Pro | Leu | Arg | Arg | Arg | Ile | Ser | Leu | Arg | Leu | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Tyr | Ala | Val | Leu | Gly | Ile | Trp | Ala | Leu | Ser | Ala | Val | Leu | Ala | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Ala | Ala | Val | His | Thr | Tyr | His | Val | Glu | Leu | Lys | Pro | His | Asp | Val |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Leu | Cys | Glu | Glu | Phe | Trp | Gly | Ser | Gln | Glu | Arg | Gln | Arg | Gln | Ile |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Tyr | Ala | Trp | Gly | Leu | Leu | Leu | Gly | Thr | Tyr | Leu | Leu | Pro | Leu | Leu | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ile | Leu | Leu | Ser | Tyr | Val | Arg | Val | Ser | Val | Lys | Leu | Arg | Asn | Arg | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Pro | Gly | Ser | Val | Thr | Gln | Ser | Gln | Ala | Asp | Trp | Asp | Arg | Ala | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Arg | Arg | Thr | Phe | Cys | Leu | Leu | Val | Val | Val | Val | Val | Val | Val | |
| | | | 115 | | | | 120 | | | | | | 125 | | |

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC   60
AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT   120
GCCTTCGAGC CACGCGGCTG GGTGTTCTGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG   180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGGTAC   240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC                               273
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG   60
GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC   120
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG     177
```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1110

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ATGGCCTCAT | CGACCACTCG | GGGCCCCAGG | GTTTCTGACT | TATTTTCTGG | GCTGCCGCCG | 60 |
| GCGGTCACAA | CTCCCGCCAA | CCAGAGCGCA | GAGGCCTCGG | CGGGCAACGG | GTCGGTGGCT | 120 |
| GGCGCGGACG | CTCCAGCCGT | CACGCCCTTC | CAGAGCCTGC | AGCTGGTGCA | TCAGCTGAAG | 180 |
| GGGCTGATCG | TGCTGCTCTA | CAGCGTCGTG | GTGGTCGTGG | GGCTGGTGGG | CAACTGCCTG | 240 |
| CTGGTGCTGG | TGATCGCGCG | GGTGCGCCGG | CTGCACAACG | TGACGAACTT | CCTCATCGGC | 300 |
| AACCTGGCCT | TGTCCGACGT | GCTCATGTGC | ACCGCCTGCG | TGCCGCTCAC | GCTGGCCTAT | 360 |
| GCCTTCGAGC | CACGCGGCTG | GGTGTTCCGG | GGCGGCCTGT | GCCACCTGGT | CTTCTTCCTG | 420 |
| CAGCCGGTCA | CCGTCTATGT | GTCGGTGTTT | ACGCTCACCA | CCATCGCAGT | GGACCGCTAC | 480 |
| GTCGTGCTGG | TGCACCCGCT | GAGGCGGCGC | ATCTCGCTGC | GCCTCAGCGC | CTACGCTGTG | 540 |
| CTGGCCATCT | GGGCGCTGTC | CGCGGTGCTG | GCGCTGCCCG | CCGCCGTGCA | CACCTATCAC | 600 |
| GTGGAGCTCA | AGCCGCACGA | CGTGCGCCTC | TGCGAGGAGT | TCTGGGGCTC | CCAGGAGCGC | 660 |
| CAGCGCCAGC | TCTACGCCTG | GGGGCTGCTG | CTGGTCACCT | ACCTGCTCCC | TCTGCTGGTC | 720 |
| ATCCTCCTGT | CTTACGTCCG | GGTGTGAGTG | AAGCTCCGCA | ACCGCGTGGT | GCCGGGCTGC | 780 |
| GTGACCCAGA | GCCAGGCCGA | CTGGGACCGC | GCTCGGCGCC | GGCGCACCTT | CTGCTTGCTG | 840 |
| GTGGTGGTCG | TGGTGGTGTT | CGCCGTCTGC | TGGCTGCCGC | TGCACGTCTT | CAACCTGCTG | 900 |
| CGGGACCTCG | ACCCCCACGC | CATCGACCCT | TACGCCTTTG | GGCTGGTGCA | GCTGCTCTGC | 960 |
| CACTGGCTCG | CCATGAGTTC | GGCCTGCTAC | AACCCCTTCA | TCTACGCCTG | GCTGCACGAC | 1020 |
| AGCTTCCGCG | AGGAGCTGCG | CAAAGTGTTG | GTCGCTTGGC | CCCGCAAGAT | AGCCCCCAT | 1080 |
| GGCCAGAATA | TGACCGTCAG | CGTGGTCATC | | | | 1110 |

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGACGAATTT CCTCATCGGC   60
AACCTGGCCT TGTCCGACGT GTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT   120
GCCTTCGAGC CACGCGGCTG GGTGTTCCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG   180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTT ACGCTCACCA CCATCGCAGT GGACCGCTAC   240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG   300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCC CCGCCGTGCA CACCTATCAC   360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC   420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC   480
ATCCTCCTGT CTTACGCCCC GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC   540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG   600
GTGGTGGTCG TGGTGGTG                                     618
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG   60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT   120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC   180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC   240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC   300
```


GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360
 GTGGTGGTGG TGGTAGTG 378

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | His | Val | Ile | Phe | Lys | Asn | Gln | Arg | Met | His | Ser | Ala | Thr | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Leu | Phe | Ile | Val | Asn | Leu | Ala | Val | Ala | Asp | Ile | Met | Ile | Thr | Leu | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Thr | Pro | Phe | Thr | Leu | Val | Arg | Phe | Val | Asn | Ser | Thr | Trp | Ile | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Lys | Gly | Met | Cys | His | Val | Ser | Arg | Phe | Ala | Gln | Tyr | Cys | Ser | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| His | Val | Ser | Ala | Leu | Thr | | | | | | | | | | |
| 65 | | | | | 70 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Ala | Asp | Leu | Phe | Trp | Lys | Asn | Leu | Asp | Leu | Pro | Thr | Phe | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Leu | Asn | Ile | Leu | Pro | Leu | Leu | Ile | Ile | Ser | Val | Ala | Tyr | Val | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Thr | Lys | Lys | Leu | Trp | Leu | Cys | Asn | Met | Ile | Val | Asp | Val | Thr | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Gln | Tyr | Phe | Ala | Leu | Arg | Pro | Lys | Lys | Lys | Lys | Thr | Ile | Lys | Met |
| | 50 | | | | | 55 | | | | | 60 | | | | |

Leu Met Leu Val Val Val Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

| | |
|---|-----|
| GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC | 60 |
| AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCTTCAC TTTGGTTCGC | 120 |
| TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG | 180 |
| TACTGCTCAC TGCACGTCTC AGCACTGACA | 210 |

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

| | |
|--|-----|
| GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTCAACATC | 60 |
| CTGCCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAACT GTGGCTGTGT | 120 |
| AATATGATTG TCGATGTGAC CACAGAGCAG TACTTTGCCC TGC GGCCCAA AAAGAAGAAG | 180 |
| ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC | 213 |

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Trp | His | Lys | Arg | Gly | Gly | Arg | Arg | Ala | Ala | Trp | Val | Val | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Gly | Val | Val | Trp | Leu | Ala | Val | Thr | Ala | Gln | Cys | Leu | Pro | Thr | Ala | Val |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Phe | Ala | Ala | Thr | Gly | Ile | Gln | Arg | Asn | Arg | Thr | Val | Cys | Tyr | Asp | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Pro | Pro | Ile | Leu | Ser | Thr | Arg | Tyr | Leu | Pro | Tyr | Gly | Met | Ala | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Val | Ile | Gly | Phe | Leu | Leu | Pro | Phe | Ile | Ala | Leu | Leu | Ala | Cys | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Arg | Met | Ala | Arg | Arg | Leu | Cys | Arg | Gln | Asp | Gly | Pro | Ala | Gly | Pro |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Ala | Gln | Glu | Arg | Arg | Ser | Lys | Ala | Ala | Arg | Met | Ala | Val | Val | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Ala | Val | | | | | | | | | | | | | |
| | | 115 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Asp | Asn | Gly | Thr | Ile | Gln | Ala | Pro | Gly | Leu | Pro | Pro | Thr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Thr | Cys | Val | Tyr | Arg | Glu | Asp | Phe | Lys | Arg | Leu | Leu | Leu | Thr | Pro | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Ser | Val | Val | Leu | Val | Val | Gly | Leu | Pro | Leu | Asn | Ile | Cys | Val | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Gln | Ile | Cys | Ala | Ser | Arg | Arg | Thr | Leu | Thr | Arg | Ser | Ala | Val | Tyr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Thr | Leu | Asn | Leu | Ala | Leu | Ala | Asp | Leu | Met | Tyr | Ala | Cys | Ser | Leu | Pro | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Leu | Ile | Tyr | Asn | Tyr | Ala | Arg | Gly | Asp | His | Trp | Pro | Phe | Gly | Asp | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Leu | Ala | Cys | Arg | Phe | Val | Arg | Phe | Leu | Phe | Tyr | Ala | Asn | Leu | His | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ser | Ile | Leu | Phe | Leu | Thr | Cys | Ile | Ser | Phe | Gln | Arg | Tyr | Leu | Gly | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Cys | His | Pro | Leu | Ala | Ser | Trp | His | Lys | Arg | Gly | Gly | Arg | Arg | Ala | Ala | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Trp | Val | Val | Cys | Gly | Val | Val | Trp | Leu | Ala | Val | Thr | Ala | Gln | Cys | Leu | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Pro | Thr | Ala | Val | Phe | Ala | Ala | Thr | Gly | Ile | Gln | Arg | Asn | Arg | Thr | Val | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Cys | Tyr | Asp | Leu | Ser | Pro | Pro | Ile | Leu | Ser | Thr | Arg | Tyr | Leu | Pro | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Gly | Met | Ala | Leu | Thr | Val | Ile | Gly | Phe | Leu | Leu | Pro | Phe | Ile | Ala | Leu | |
| | 195 | | | | | | 200 | | | | | 205 | | | | |
| Leu | Ala | Cys | Tyr | Cys | Arg | Met | Ala | Arg | Arg | Leu | Cys | Arg | Gln | Asp | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Ala | Gly | Pro | Val | Ala | Gln | Glu | Arg | Arg | Ser | Lys | Ala | Ala | Arg | Met | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Ala | Val | Val | Val | Ala | Ala | Val | Phe | Ala | Ile | Ser | Phe | Leu | Pro | Phe | His | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Thr | Lys | Thr | Ala | Tyr | Leu | Ala | Val | Arg | Ser | Thr | Pro | Gly | Val | Ser | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Cys | Pro | Val | Leu | Glu | Thr | Phe | Ala | Ala | Ala | Tyr | Lys | Gly | Thr | Arg | Pro | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Phe | Ala | Ser | Val | Asn | Ser | Val | Leu | Asp | Pro | Ile | Leu | Phe | Tyr | Phe | Thr | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Gln | Gln | Lys | Phe | Arg | Arg | Gln | Pro | His | Asp | Leu | Leu | Gln | Arg | Leu | Thr | |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| Ala | Lys | Trp | Gln | Arg | Gln | Arg | Val | | | | | | | | | |
| | | | | 325 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60
CTGGCTGTGA CAGCCCAGTG CCTGCCCACG GCAGTCTTTG CTGCCACAGG CATCCAGCGC 120
AACCGCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT 180
GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT 240
TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGGTCCTGT GGCCCAAGAG 300
CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

T CGGTGGTGCT GGTGGTCGGC 120
CTGCCACTGA ACATCTGCGT CATTGCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180
TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTCACTACCC 240
CTACTTATCT ATAACCTACGC CAGAGGGGAC CACTGGCCCT TCGGAGACCT CGCCTGCCGC 300
TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTCTT CACCTGCATT 360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT 420

| | |
|--|-----|
| CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG | 480 |
| CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG | 540 |
| AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTCATCGGC | 600 |
| TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTTATTGTC GCATGGCCCG CCGCCTGTGT | 660 |
| CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAGCAAGGC GGCTCGTATG | 720 |
| GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA | 780 |
| GCCTACTTGG CTGTGCGCTC CACGCCCGGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT | 840 |
| GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCAACA GTGTTCTGGA CCCCATTCCTC | 900 |
| TTCTACTTCA CACAACAGAA GTTCCGGCGG CAACCCACG ATCTCTTACA GAGGCTCACA | 960 |
| GCCAAGTGGC AGAGGCAGAG AGTC | 984 |

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Ala | Met | Ser | Val | Asp | Arg | Tyr | Val | Ala | Ile | Val | His | Ser | Arg | Arg | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ser | Ser | Ser | Leu | Arg | Val | Ser | Arg | Asn | Ala | Leu | Leu | Gly | Val | Gly | Phe | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Trp | Ala | Leu | Ser | Ile | Ala | Met | Ala | Ser | Pro | Val | Ala | Tyr | His | Gln | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Arg | Leu | Phe | His | Arg | Asp | Ser | Asn | Gln | Thr | Phe | Cys | Trp | Glu | Gln | Trp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Pro | Asn | Lys | Leu | His | Lys | Lys | Ala | Tyr | Val | Val | Cys | Thr | Phe | Val | Phe | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Gly | Tyr | Leu | Leu | Pro | Leu | Leu | Leu | Ile | Cys | Phe | Cys | Tyr | Ala | Lys | Val | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| Leu | Asn | His | Leu | His | Lys | Lys | Leu | Lys | Asn | Met | Ser | Lys | Lys | Ser | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ala | Ser | Lys | Lys | Lys | Thr | Ala | Gln | Thr | Val | Leu | Val | Val | Val | Val | Val | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTGTGCACT CGCGGCGCTC CTCCTCCCTC      60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGGCGCTGTC CATCGCCATG      120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACAGCAACCA GACCTTCTGC      180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT      240
GGGTACCTTC TGCCCTTACT GCTCATCTGC TTTTGCTATG CCAAGGTCCT TAATCATCTG      300
CATAAAAAGC TGAAAAACAT GTCAAAAAG TCTGAAGCAT CCAAGAAAAA GACTGCACAG      360
ACCGTCCTGG TGGTCGTTGT AGTA                                           384
```

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val
 1              5              10              15
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys
      20              25              30
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala
      35              40              45
His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val
      50              55              60
Ala Gly Val Ser Leu Leu Pro
```

65

70

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCCT TCTCCGTCTA CTCCTGCAC 60
 CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTTCCTCCCT GCTGAACGCC 120
 GGCGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCGGGT GCTGGGGCTC 180
 TGC GCCTTCG TGGCGGGCGT GAGCCTCCTG CCGGC 215

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1 5 10 15
 Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu
 20 25 30
 Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val
 35 40 45
 Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly
 50 55 60
 Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala
 65 70 75 80
 Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr
 85 90 95
 Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His
 100 105 110

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Tyr | Phe | Phe | Thr | Val | Ser | Met | Leu | Val | Ser | Ile | Phe | Thr | Leu | Ala | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Met | Ser | Val | Asp | Arg | Tyr | Val | Ala | Ile | Val | His | Ser | Arg | Arg | Ser | Ser | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ser | Leu | Arg | Val | Ser | Arg | Asn | Ala | Leu | Leu | Gly | Val | Gly | Phe | Ile | Trp | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ala | Leu | Ser | Ile | Ala | Met | Ala | Ser | Pro | Val | Ala | Tyr | His | Gln | Arg | Leu | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| Phe | His | Arg | Asp | Ser | Asn | Gln | Thr | Phe | Cys | Trp | Glu | Gln | Trp | Pro | Asn | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Lys | Leu | His | Lys | Lys | Ala | Tyr | Val | Val | Cys | Thr | Phe | Val | Phe | Gly | Tyr | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Leu | Leu | Pro | Leu | Leu | Leu | Ile | Cys | Phe | Cys | Tyr | Ala | Lys | Val | Leu | Asn | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| His | Leu | His | Lys | Lys | Leu | Lys | Asn | Met | Ser | Lys | Lys | Ser | Glu | Ala | Ser | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Lys | Lys | Lys | Thr | Ala | Gln | Thr | Val | Leu | Val | Val | Val | Val | Val | Phe | Gly | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Ser | Trp | Leu | Pro | His | His | Val | Val | His | Leu | Trp | Ala | Glu | Phe | Gly | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ala | Phe | Pro | Leu | Thr | Pro | Ala | Ser | Phe | Phe | Phe | Arg | Ile | Thr | Ala | His | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Cys | Leu | Ala | Tyr | Ser | Asn | Ser | Ser | Val | Asn | Pro | Ile | Ile | Tyr | Ala | Phe | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Leu | Ser | Glu | Asn | Phe | Arg | Lys | Ala | Tyr | Lys | Gln | Val | Phe | Lys | Cys | His | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Val | Cys | Asp | Glu | Ser | Pro | Arg | Ser | Glu | Thr | Lys | Glu | Asn | Lys | Ser | Arg | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Met | Asp | Thr | Pro | Pro | Ser | Thr | Asn | Cys | Thr | His | Val | | | | | |
| | | | 340 | | | | | 345 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1044
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

| | | | | | | | | | | | | | |
|--------|--------|-----------|------|---------|-------|----------|--------|---------|--------|---------|--------|------|-----|
| ATGGA | ACTGG | CTATGG | TGAA | CCTCAG | TGAA | GGGAAT | GGGA | GCGACCC | CAGA | GCCGCC | CAGCC | 60 | |
| CCGGAG | TCCA | GGCCGCT | CCTT | CGGCATT | GGC | GTGGAGA | AACT | TCATTAC | GCT | GGTAGT | GTTT | 120 | |
| GGCCTG | ATTT | TCGCGAT | GGG | CGTGCT | GGGC | AACAGCCT | TGG | TGATCAC | CGT | GCTGGC | GCGC | 180 | |
| AGCAA | ACCAG | GCAACCCCC | G | CAGCACC | ACC | AACCTGT | TTA | TCCTCA | AATCT | GAGCAT | CGCA | 240 | |
| GACCTG | GCCT | ACCTGCT | CCTT | CTGCAT | CCCT | TTTCAGG | CCA | CCGTGT | ATGC | ACTGCCC | ACC | 300 | |
| TGGGTG | CTGG | GCGCCTT | CAT | CTGCAAG | TTT | ATACACT | ACT | TCTTCAC | CGT | GTCCAT | GCTG | 360 | |
| GTGAG | CATCT | TCACCCT | TGGC | CGCGAT | GTCT | GTGGAT | CGCT | ACGTGG | CCAT | TGTGCA | CTCG | 420 | |
| CGGCG | CTCCT | CCTCCCT | CAG | GGTGT | CCCCG | C | AACGCA | CTGC | TGGGCG | TGGG | CTTCAT | CTGG | 480 |
| GCGCTG | TCCA | TCGCCAT | TGGC | CTCGCC | GGTG | GCCTACC | ACC | AGCGTCT | TTTT | CCATCG | GGGAC | 540 | |
| AGCAA | ACCAGA | CCTTCTG | CTG | GGAGCAG | TGG | CCCAACA | AGC | TCCACA | AAGAA | GGCTTAC | GTG | 600 | |
| GTGTG | CACTT | TCGTCTT | TGG | GTACCTT | CTG | CCCTTAC | TGC | TCATCTG | CCTT | TTGCTAT | GCC | 660 | |
| AAGGT | CCTTA | ATCATCT | GCA | TAAAA | AGCTG | AAAAA | CATGT | CAAAAA | AGTC | TGAAG | CATCC | 720 | |
| AAGAAA | AAGA | CTGCAC | AGAC | CGTCCT | TGGTG | GTCGTT | GTAG | TATTTG | GCA | ATCCTG | GCTG | 780 | |
| CCCCAT | CATG | TCGTCC | ACCT | CTGGG | CTGAG | TTTGG | AGCCT | TCCCAC | TGAC | GCCAG | CTTC | 840 | |
| TTCTT | CTTCA | GAATCAC | CGC | CCATTG | CCTG | GCATAC | AGCA | ACTCCT | CAGT | GAACCCC | ATC | 900 | |
| ATATAT | GCCT | TTCTCT | CAGA | AAACTT | CCGG | AAGGCG | TACA | AGCAAG | TGTT | CAAGTG | TCAT | 960 | |
| GTTTG | CGATG | AATCTC | CACG | CAGTGAA | AACT | AAGGAAA | ACA | AGAGCC | GGAT | GGACAC | CCCCG | 1020 | |
| CCATCC | ACCA | ACTGCAC | CCA | CGTG | | | | | | | | 1044 | |

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Thr | Leu | His | Pro | Val | Trp | Ser | Gln | Lys | His | Arg | Thr | Ser | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Ser | Arg | Val | Val | Leu | Gly | Val | Trp | Leu | Ser | Ala | Thr | Ala | Phe |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Ser | Val | Pro | Tyr | Leu | Val | Phe | Arg | Glu | Thr | Tyr | Asp | Asp | Arg | Lys | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Val | Thr | Cys | Arg | Asn | Asn | Tyr | Ala | Val | Ser | Thr | Asp | Trp | Glu | Ser |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Lys | Glu | Met | Gln | Thr | Val | Arg | Gln | Trp | Ile | His | Ala | Thr | Cys | Phe | Ile |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Arg | Phe | Ile | Leu | Gly | Phe | Leu | Leu | Pro | Phe | Leu | Val | Ile | Gly | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Cys | Tyr | Glu | Arg | Val | Ala | Arg | Lys | Met | Lys | Glu | Arg | Gly | Leu | Phe | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Lys | Pro | Phe | Lys | Val | Thr | Met | Thr | Ala | Val | Ile | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | |

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTTCTCACCC | TTCACCCAGT | GTGGTCCCAA | AAGCACCGAA | CCTCACACTG | GGCTTCCAGA | 60 |
| GTCGTTCTGG | GAGTCTGGCT | CTCTGCCACT | GCCTTCAGCG | TGCCCTATTT | GGTTTTTCAGG | 120 |
| GAGACATATG | ATGACCGTAA | AGGAAGAGTG | ACCTGCAGAA | ATAACTACGC | TGTGTCCACT | 180 |
| GACTGGGAAA | GCAAAGAGAT | GCAAACAGTA | AGACAATGGA | TTCATGCCAC | CTGTTTCATC | 240 |
| AGCCGCTTCA | TACTGGGCTT | CCTTCTGCCT | TTCTTAGTCA | TTGGCTTTTG | TTATGAAAGA | 300 |
| GTAGCCCGCA | AGATGAAAGA | GAGGGGCCTC | TTTAAATCCA | GCAAACCCTT | CAAAGTCACG | 360 |
| ATGACTGCTG | TTATCTC | | | | | 377 |

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn
1 5 10 15
Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu
20 25 30
Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr
35 40 45
Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His
50 55 60
Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu
65 70 75 80
Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser
85 90 95
His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Lys Ser Ser
100 105 110
Arg Asn Ile Phe Ser Ile Val
115

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAAGATTG TGAAGCCCCT TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAACCTC 60
GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCCCAACGT CATTCTCACC 120
AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACTTAAAAA CGAACTGGGC 180
CGCCAGTGGC ACAAGGCGTC AAACCTACATC TTTGTGGGCA TTTTCTGGCT TGTGTTTCCTT 240

TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCCA CCTGAAATCC 300
 AGAAAGAATT CCATCTCGGT CAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Leu | Leu | Ala | Ala | Leu | Thr | Leu | Met | Pro | Leu | Ala | Met | Leu | Ser | 1 | 5 | 10 | 15 |
| Ser | Ser | Ala | Leu | Phe | Asp | His | Ala | Leu | Phe | Gly | Glu | Val | Ala | Cys | Arg | 20 | 25 | 30 | |
| Leu | Tyr | Leu | Phe | Leu | Ser | Val | Cys | Phe | Val | Ser | Leu | Ala | Ile | Leu | Ser | 35 | 40 | 45 | |
| Val | Ser | Ala | Ile | Asn | Val | Glu | Arg | Tyr | Tyr | Tyr | Val | Val | His | Pro | Met | 50 | 55 | 60 | |
| Arg | Tyr | Glu | Val | Arg | Met | Lys | Leu | Gly | Leu | Val | Ala | Ser | Val | Leu | Val | 65 | 70 | 75 | 80 |
| Gly | Val | Trp | Val | Lys | Ala | Leu | Ala | Met | Ala | Ser | Val | Pro | Val | Leu | Gly | 85 | 90 | 95 | |
| Arg | Val | Ser | Trp | Glu | Glu | Gly | Pro | Pro | Ser | Val | Pro | Pro | Gly | Cys | Ser | 100 | 105 | 110 | |
| Leu | Gln | Trp | Ser | His | Ser | Ala | Tyr | Cys | Gln | Leu | Phe | Val | Val | Val | Phe | 115 | 120 | 125 | |
| Ala | Val | Leu | Tyr | Phe | Leu | Leu | Pro | Leu | Leu | Leu | Ile | Leu | Val | Val | Tyr | 130 | 135 | 140 | |
| Cys | Ser | Met | Phe | Arg | Val | Ala | Arg | Val | Ala | Ala | Met | Gln | His | Gly | Pro | 145 | 150 | 155 | 160 |
| Leu | Pro | Thr | Trp | Met | Glu | Thr | Pro | Arg | Gln | Arg | Ser | Glu | Ser | Leu | Ser | 165 | 170 | 175 | |
| Ser | Arg | Ser | Thr | Met | Val | Thr | Ser | Ser | Gly | Ala | Pro | Gln | Thr | Thr | Pro | 180 | 185 | 190 | |
| His | Arg | Thr | Phe | Gly | Gly | Gly | Lys | Ala | Ala | Val | Val | Leu | Leu | Ala | Val | 195 | 200 | 205 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Gln | Phe | Leu | Leu | Cys | Trp | Leu | Pro | Tyr | Phe | Ser | Phe | His | Leu |
| 210 | | | | | | 215 | | | | | 220 | | | | |
| Tyr | Val | Ala | Leu | Ser | Ala | Gln | Pro | Ile | Ala | Ala | Gly | Gln | Val | Glu | Asn |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Val | Val | Thr | Trp | Ile | Gly | Tyr | Phe | Cys | Phe | Thr | Ser | | | | |
| | | | | 245 | | | | | 250 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GTGGACCTGC | TGGCTGCCCT | GACCCTCATG | CCTCTGGCCA | TGCTCTCCAG | CTCCGCCCTC | 60 |
| TTTGACCACG | CCCTCTTTGG | GGAGGTGGCC | TGCCGCCTCT | ACTTGTTTCCT | GAGCGTCTGC | 120 |
| TTTGTCAGCC | TGGCCATCCT | CTCGGTGTCC | GCCATCAATG | TGGAGCGCTA | CTATTATGTG | 180 |
| GTCCACCCCA | TGCGCTATGA | GGTGCGCATG | AAACTGGGGC | TGGTGGCCTC | TGTGCTGGTG | 240 |
| GGCGTGTGGG | TGAAGGCCCT | GGCCATGGCT | TCTGTGCCAG | TGTTGGGAAG | GGTGTCTTGG | 300 |
| GAGGAAGGCC | CTCCCAGTGT | CCCCCAGGC | TGTTCACTCC | AATGGAGCCA | CAGTGCCTAC | 360 |
| TGCCAGCTTT | TCGTGGTGGT | CTTCGCCGTC | CTCTACTTCC | TGCTGCCCCT | GCTCCTCATC | 420 |
| CTTGTGGTCT | ACTGCAGCAT | GTTCCGGGTG | GCTCGTGTGG | CTGCCATGCA | GCACGGGCCG | 480 |
| CTGCCCACGT | GGATGGAGAC | GCCCCGGCAA | CGCTCCGAGT | CTCTCAGCAG | CCGCTCCACT | 540 |
| ATGGTCACCA | GCTCGGGGGC | CCCGCAGACC | ACCCCTCACC | GGACGTTTGG | CGGAGGGAAG | 600 |
| GCAGCAGTGG | TCCTCCTGGC | TGTGGGAGGA | CAGTTCCTGC | TCTGTTGGTT | GCCCTACTTC | 660 |
| TCCTTCCACC | TCTATGTGGC | CCTGAGCGCT | CAGCCCATTG | CAGCGGGGCA | GGTGGAGAAC | 720 |
| GTGGTGACCT | GGATTGGCTA | CTTCTGCTTC | ACCTCC | | | 756 |

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

GCCGATGTGC TGGTGACAGC CATCTGCCTG CCGGCCAGTC TGCTGGTAGA CATCACGGAA    60
TCCTGGCTCT TTGGCCATGC CCTCTGCAAG GTCATCCCCT ATCTACAGGC CGTGTCCTGT    120
TCAGTGGTCG TGCTGACTCT CAGCTCCATC GCCCTGGACC GCTGGTACGC CATCTGCCAC    180
CCGCTGTTGT TCAAGAGCAC TGCCCGGCGC GCCCGCGGCT CCATCCTCGG CATCTGGGCG    240
GTGTCGCTGG CTGTCATGGT GCCTCAGGCT GCTGTCATGG AGTGTAGCAG CGTGCTGCCC    300
GAGCTGGCCA ACCGCACCCG CCTCCTGTCT GTCTGTGATG AGCGCTGGGC AGACGACCTG    360
TACCCCAAGA TCTACCACAG CTGCTTCTTC ATTGTCACCT ACCTGGCCCC ACTGGGCCTC    420
ATGGCCATGG CCTATTTCCA GATCTTCCGC AAGCTCTGGG GCCGCCAGAT CCCCGGCACC    480
ACCTCGGCCC TGGTGCGCAA CTGGAAGCGG CCCTCAGACC AGCTGGACGA CCAGGGCCAG    540
GGCCTGAGCT CAGAGCCCCA GCCCCGGGCC CGCGCCTTCC TGGCCGAGGT GAAACAGATG    600
CGAGCCCGGA GGAAGACGGC CAAGATGCTG ATGGTGGTGC TGCTGGTCTT CGCCCTCTGC    660
TACCTGCCCC TCAGTGTCTT CAACGTCCTC AAGAGGGTCT TCGGGATGTT CCGCCAAGCC    720
AGCGACCGAG AGGCCATCTA CGCCTGCTTC ACCTTCTCCC ACTGGCTGGT GTACGCCAAC    780
AGCGCCGCC                                     789
  
```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328
 (B) TYPE: Amino acid
 (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Trp | Asp | Asn | Gly | Thr | Gly | Gln | Ala | Leu | Gly | Leu | Pro | Pro | Thr | |
| 1 | | | | 5 | | | | | 10 | | | | | | 15 | |
| Thr | Cys | Val | Tyr | Arg | Glu | Asn | Phe | Lys | Gln | Leu | Leu | Leu | Pro | Pro | Val | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Ser | Ala | Val | Leu | Ala | Ala | Gly | Leu | Pro | Leu | Asn | Ile | Cys | Val | Ile | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Thr | Gln | Ile | Cys | Thr | Ser | Arg | Arg | Ala | Leu | Thr | Arg | Thr | Ala | Val | Tyr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Thr | Leu | Asn | Leu | Ala | Leu | Ala | Asp | Leu | Leu | Tyr | Ala | Cys | Ser | Leu | Pro | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Leu | Ile | Tyr | Asn | Tyr | Ala | Gln | Gly | Asp | His | Trp | Pro | Phe | Gly | Asp | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Phe | Ala | Cys | Arg | Leu | Val | Arg | Phe | Leu | Phe | Tyr | Ala | Asn | Leu | His | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ser | Ile | Leu | Phe | Leu | Thr | Cys | Ile | Ser | Phe | Gln | Arg | Tyr | Leu | Gly | Ile | |
| | 115 | | | | | | 120 | | | | | 125 | | | | |
| Cys | His | Pro | Leu | Ala | Pro | Trp | His | Lys | Arg | Gly | Gly | Arg | Arg | Ala | Ala | |
| 130 | | | | | | 135 | | | | | 140 | | | | | |
| Trp | Leu | Val | Cys | Val | Thr | Val | Trp | Leu | Ala | Val | Thr | Thr | Gln | Cys | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Pro | Thr | Ala | Ile | Phe | Ala | Ala | Thr | Gly | Ile | Gln | Arg | Asn | Arg | Thr | Val | |
| | | | 165 | | | | | | 170 | | | | | 175 | | |
| Cys | Tyr | Asp | Leu | Ser | Pro | Pro | Ala | Leu | Ala | Thr | His | Tyr | Met | Pro | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Gly | Met | Ala | Leu | Thr | Val | Ile | Gly | Phe | Leu | Leu | Pro | Phe | Ala | Ala | Leu | |
| | 195 | | | | | | 200 | | | | | 205 | | | | |
| Leu | Ala | Cys | Tyr | Cys | Leu | Leu | Ala | Cys | Arg | Leu | Cys | Arg | Gln | Asp | Gly | |
| 210 | | | | | 215 | | | | | | 220 | | | | | |
| Pro | Ala | Glu | Pro | Val | Ala | Gln | Glu | Arg | Arg | Gly | Lys | Ala | Ala | Arg | Met | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Ala | Val | Val | Val | Ala | Ala | Ala | Phe | Ala | Ile | Ser | Phe | Leu | Pro | Phe | His | |
| | | | 245 | | | | | | 250 | | | | | 255 | | |
| Ile | Thr | Lys | Thr | Ala | Tyr | Leu | Ala | Val | Gly | Ser | Thr | Pro | Gly | Val | Pro | |
| | | 260 | | | | | | 265 | | | | | 270 | | | |
| Cys | Thr | Val | Leu | Glu | Ala | Phe | Ala | Ala | Ala | Tyr | Lys | Gly | Thr | Arg | Pro | |
| | | 275 | | | | 280 | | | | | | 285 | | | | |

Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
 290 295 300
 Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr
 305 310 315 320
 Ala Lys Trp Gln Arg Gln Gly Arg
 325

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 984
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

| | |
|---|-----|
| ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGCTTGC CACCCACCAC CTGTGTCTAC | 60 |
| CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GCGGCTGGC | 120 |
| CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCGCCGGGC CCTGACCCGC | 180 |
| ACGGCCGTGT ACACCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCCTGCCC | 240 |
| CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGGCGACTT CGCCTGCCGC | 300 |
| CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCTCTTCCT CACCTGCATC | 360 |
| AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGGCACAA ACGTGGGGGC | 420 |
| CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG | 480 |
| CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC | 540 |
| AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTCATCGGC | 600 |
| TTCTTGCTGC CCTTTGCTGC CCTGCTGGCC TGCTACTGTC TCCTGGCCTG CCGCCTGTGC | 660 |
| CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGGCAAGGC GGCCCGCATG | 720 |
| GCCGTGGTGG TGGCTGCTGC CTTTGCCATC AGCTTCCTGC CTTTTCACAT CACCAAGACA | 780 |
| GCCTACCTGG CAGTGGGCTC GACGCCGGGC GTCCCCTGCA CTGTATTGGA GGCCTTTGCA | 840 |
| GCGGCCTACA AAGGCACGCG GCCGTTTGCC AGTGCCAACA GCGTGCTGGA CCCCATCCTC | 900 |
| TTCTACTTCA CCCAGAAGAA GTTCCGCCGG CGACCACATG AGCTCCTACA GAAACTCACA | 960 |

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ACAGCCATCT TCGTGCCAC AGGCAT 26

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

AGACAGTAGC AGGCCAGCAG GGCAGCAAA 29

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC 27

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA

29

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Cont
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